

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: PERSSON, MATS AXEL
ALLANDER, TOBIAS ERIK
- (ii) TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
HEPATITIS C VIRUS (HCV) E2 ANTIGEN
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: ROBINS & ASSOCIATES
 - (B) STREET: 90 MIDDLEFIELD ROAD, SUITE 200
 - (C) CITY: MENLO PARK
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94025
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/844,215
 - (B) FILING DATE: 17-APR-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/635,109
 - (B) FILING DATE: 19-APR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MCCRACKEN, THOMAS P.
 - (B) REGISTRATION NUMBER: 38,548
 - (C) REFERENCE/DOCKET NUMBER: 80146.002
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (650) 325-7812
 - (B) TELEFAX: (650) 325-7823

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Val Arg Lys Pro Gly
1 5 10 15

Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Gly
20 25 30

His Val Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
35 40 45

Met Gly Glu Ser Ile Pro Ile Phe Gly Ser Ala Asn Tyr Ala Gln Asn
50 55 60

Tyr Ala Gln Lys Phe Arg Asp Arg Val Ser Ile Ile Ala Asp Glu Ser
65 70 75 80

Thr Ser Thr Ser Phe Ile Glu Leu Ser Asn Leu Arg Ser Asp Asp Thr
85 90 95

Ala Val Tyr Tyr Cys Ala Arg Asp Pro Pro Arg Tyr Cys Ser Ala Gly
100 105 110

Arg Cys Tyr Pro Gly Phe Phe Gln Gln Trp Gly Gln Gly Thr Leu Val
115 120 125

Thr Val Ser Ser
130

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1 5 10 15

Ser Ser Val Lys Val Ser Cys Gln Val Phe Gly Asp Thr Phe Ser Arg
20 25 30

Tyr Thr Ile Gln Trp Leu Arg Gln Ala Pro Gly Gln Gly Pro Glu Trp
35 40 45

Met Gly Asn Ile Ile Pro Val Tyr Asn Thr Pro Asn Tyr Ala Gln Lys
50 55 60

Phe Gln Gly Arg Leu Ser Ile Thr Ala Asp Asp Ser Thr Ser Thr Ala
65 70 75 80

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe
85 90 95

Cys Ala Arg Val Val Ile Pro Asn Ala Ile Arg His Thr Met Gly Tyr
100 105 110

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1 5 10 15

Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Gly
20 25 30

His Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
35 40 45

Met Gly Gly Ser Ile Ser Phe Phe Gly Thr Ser Asn Ser Ala Gln Lys
50 55 60

Phe Gln Gly Arg Val Ser Ile Thr Ala Asp Glu Ser Ala Ser Thr Ala
65 70 75 80

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr
85 90 95

Cys Ala Lys Asp Pro Pro Arg Phe Cys Ser Gly Gly Asn Cys Tyr Pro
100 105 110

Gly Phe Phe Gln Gln Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Val Gln Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Thr Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala	Gly	Ile	Ser	Phe	Asp	Gly	Ser	Asn	Gln	Tyr	Tyr	Ala	Asp	Ser	Val
50						55				60					
Lys	Gly	Arg	Phe	Ile	Val	Ser	Arg	Asp	Asn	Ser	Arg	Asp	Thr	Val	Phe
65					70				75			80			
Leu	Gln	Met	Ser	Ser	Leu	Arg	Leu	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85				90					95		
Ala	Thr	Glu	Gly	Ser	Pro	Phe	Gly	Ser	Ile	Lys	Gly	Arg	Tyr	Tyr	Leu
				100				105				110			
Glu	Asn	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
				115				120			125				

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5				10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ala	Tyr
				20				25				30			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
				35				40			45				
Ala	Gly	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Gln	Tyr	Tyr	Ser	Asp	Ser	Val
				50				55			60				
Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Arg	Asn	Thr	Leu	Phe
65					70				75			80			
Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85				90				95			
Ala	Thr	Glu	Val	Leu	Phe	Gly	Ser	Ile	Lys	Gly	Arg	Tyr	Tyr	Leu	Glu
				100				105			110				
Asn	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser				
				115				120							

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gly
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Arg	Ser	Ser
	20						25					30			
His	Trp	Trp	Ser	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp
	35					40					45				
Ile	Gly	Glu	Val	Phe	Phe	Ser	Gly	Ser	Thr	Ile	Tyr	Asn	Pro	Ser	Leu
	50					55				60					
Asn	Asp	Arg	Val	Phe	Met	Ser	Val	Asp	Lys	Ser	Lys	Asp	Gln	Val	Ser
	65				70				75			80			
Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
		85					90					95			
Ala	Arg	Ser	Pro	Ile	Lys	Met	Asn	Gln	Gly	Arg	Met	Met	Leu	Asp	Ala
			100				105					110			
Phe	Asp	Ile	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile	Val	Ser	Ser		
		115					120			125					

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Ser	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5					10				15		
Ser	Val	Lys	Val	Ser	Cys	Arg	Ala	Ser	Gly	Gly	Ser	Phe	Arg	Ser	Tyr
		20						25				30			
Asn	Phe	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
			35					40				45			
Gly	Gly	Ile	Ile	Pro	Met	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
			50			55				60					
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ala	Thr	Gly	Tyr
		65			70				75			80			

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85				90						95
Ala	Met	Pro	Tyr	Pro	Lys	His	Cys	Ser	Arg	Gly	Ser	Cys	Trp	Gly	Trp
					100			105					110		
Phe	Asp	Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
					115			120					125		

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala	Glu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu
1				5					10					15	
Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Asn	Tyr
					20				25					30	
Leu	Ala	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
					35			40					45		
Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro
	65				70				75					80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Leu	Tyr	Gly	Asn	Ser	Arg	Trp
					85				90					95	
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys					
					100				105						

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Glu Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
1 5 10 15

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Lys Tyr Leu
20 25 30

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asp Trp Val Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
1 5 10 15

Arg Ala Thr Leu Ser Cys Gly Ala Ser Gln Ser Val Arg Ser Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Val Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala	Glu	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly	Glu
1				5					10					15	
Arg	Ala	Ser	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Gly	Asn	Asn	Leu
	20							25					30		
Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
	35					40					45				
Gly	Gly	Asn	Thr	Arg	Ala	Thr	Gly	Thr	Pro	Asp	Arg	Phe	Ser	Gly	Ser
	50					55				60					
Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu
	65				70				75				80		
Asp	Phe	Ala	Val	Tyr	Phe	Cys	Gln	His	Tyr	Ser	Thr	Trp	Pro	Leu	Thr
		85						90					95		
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Phe	Lys						
		100					105								

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala	Glu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Val	Gly	Glu
1					5				10					15	
Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Tyr	Ser	Gly	Tyr
	20							25				30			
Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Arg	Leu	Leu	Ile
		35					40					45			
Tyr	Gly	Ala	Ser	Asn	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly
		50					55				60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Ser
	65				70				75				80		

Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Pro	Pro	Tyr
			85					90					95		
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100				105								

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala	Glu	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Phe	Val	Gly	Asp
1				5					10					15	
Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Arg	Asn	Leu
			20					25				30			
Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Thr	Ala	Pro	Lys	Val	Leu	Ile	Tyr
			35				40				45				
Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
			50				55			60					
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Thr	Ser	Leu	Gln	Pro	Glu
			65			70			75				80		
Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Thr	Thr	Pro	Arg	Thr
			85					90				95			
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Val	Lys						
			100				105								

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala	Glu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu
1					5				10				15		

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Ser Ser Lys Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Phe Ile
35 40 45

Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Arg Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Thr Pro Arg Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGCTCACGC AGTCTCCAGG CACCCTGTCT TTGTCTCCAG GGGAAAGAGC CACCCTCTCC 60
TGCAGGGCCA GTCAGAGTGT TAGCAGCAAT TACTTAGCCT GGTACCAGCA GAGACCTGGC 120
CAGGCTCCA GGCTCCTCAT CTATGGTGCA TCCAGCAGGG CCACTGGCAT CCCAGACAGG 180
TTCAGTGGCA GTGGGTCTGG GACAGACTTC ACTCTCACCA TCAGCAGACT GGAGCCTGAA 240
GATTTGCAG TGTATTACTG TCAGCTTAT GGTAACTCAC GTTGGACGTT CGGCCAAGGG 300
ACCAAGGTGG AGATCAA 318

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGCTCACTC AGTCTCCAGC CACCCTGTCT TTGTCTCCAG GGGAAAGAGC CACCCTCTCC 60

TGCAGGGCCA GTCAGAGTGT TAACAAGTAC TTAGCCTGGT ACCAACAGAA ACCTGGCCAG	120
GCTCCCAGGC TCCTCATCTA TGATGCATCC AACAGGGCCA CTGGCATCCC AGCCAGGTTC	180
AGTGGCAGTG GGTCTGGAC AGACTTCACT CTCACCATCA GCAACCTAGA GCCTGAAGAT	240
TTTGCAGTTT ATTACTGTCA GCAGCGTAGC GACTGGGTCA CTTTCGGCGG AGGGACCAAG	300
GTGGAGATCA AA	312

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAGCTCACGC AGTCTCCAGG CACCCTGTCT TTGTCTCCAG GGGAAAGAGC CACCCCTCTCC	60
TGCAGGGCCA GTCAGAGTGT TAGGAGCAAC TACTTAGCCT GGTACCAGCA AAAACCTGGC	120
CAGGCTCCA GGCTCCTCAT CTATGGTGTAA TCCAGCAGGG CCACCTGGCAT CCCAGACAGG	180
TTCAGTGGCA GTGGGTCTGG GACAGACTTC ACTCTCACCA TCAGCAGACT GGAGCCTGAA	240
GATTTTGCAG TGTATTACTG TCAGCAGTAT GGTAGCTCAC CTCGGACTTT TGGCCAGGGG	300
ACCAAGTTGG AGATCAAA	318

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGCTCACGC AGTCTCCAGC CACCCTGTCT GTGTCTCCAG GGGAAAGAGC CTCCCTCTCC	60
TGCAGGGCCA GTCAGAGTGT CGGTAACAAT TTAGCTTGGT ATCAGCAGAA ACCTGGCCAG	120
GCTCCCAGGC TCCTCATTAA TGTTGGAAAC ACCAGAGCCA CTGGTACCCC AGACAGGTTC	180
AGTGGCAGTG GGTCTGGAC AGAATTCACT CTCACCATCA GCAGCCTGCA GTCTGAGGAC	240

TTTGCAGTTT ATTTCTGTCA ACACATAGT ACCTGGCCGC TCACCTTCGG CGGGGGGACC	300
AAGGTCGAGT TCAAG	315

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAGGTGCAGC TGCTCGAGTC TGGGGGAGGC GTGGTCCAGC CTGGGAGGTC CCTGAGACTC	60
TCCTGTGCAG CGTCTGGATT CACCTTCAGT GCTTATGGCA TGCACGGGT CCGCCAGGCT	120
CCAGGCAAGG GGCTGGAGTG GGTGGCAGGT ATATGGTTG ATGGAAGTAA TCAATACTAT	180
TCAGACTCCG TGAAGGGCCG ATTCAACCGTC TCCAGAGACA ATTCCAGGAA CACGCTGTTT	240
CTGCAAATGA ACAGCCTGAG ACCCGAGGAC ACGGCTGTCT ATTACTGTGC GACAGAGGTA	300
CTTTTGAGAT CGATTAAGGG GCGTTACTAC CTTGAAAATC GGGGCCAGGG AACCCTGGTC	360
ACCGTCTCCT CA	372

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGGAGCTCA CCCAGTCTCC ATCGTCCCTG TCTGCATTTG TNGGAGACAG AGTCACCATC	60
ACTTGCCGGG CAAGTCAGAG TATTAGCAGG AACTTAAATT GGTATCAGCA GAAACCAGGG	120
ACAGCCCCTA AGGTCCCTGAT CTATGCTGCA TCCAGTTGC AAAGTGGGT CCCATCGAGG	180
TTCAGTGGCA GTGGATCTGG GACAGATTTC ACTCTCACCA TCACCAGTCT GCAACCTGAA	240
GATTTGCAA CTTACTATTG TCAACAGAGT TACACAACCC CTCGGACGTT CGGCCAAGGG	300
ACCAAGGTGG AAGTCAAA	318

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCCGAGCTCA CGCAGTCTCC AGGCACCCTG TCTTGTCTC CAGGGGAAAG AGCCACCCTC	60
TCCTGCAGGG CCAGTCAGAG TCTTAGCAGC AAATACTTAG CNTGGTACCA ACAGAAACCT	120
GGCCAGGCTC CCAGGCTCTT CATTATGAT GCATCCAGCA GGGCCACTGG CATCCCAGAC	180
AGGTTCACTG GCAGTGGTC TGGGACAGAC TTCACTCTCA GCATCAGCAG ATTGGAGCCT	240
GAAGATTTG CAGTGTATTA CTGTCAGCAG TATGGAACAC CTCGCACCTT CGGCCAGGGG	300
ACCAAGGTGG AAATCAAA	318

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCGAGCAGT CTGGGGCTGA GGTGAGGAAG CCTGGGTCT CGGTGAAGGT CTCCTGCAAG	60
GCTTCTGGAG GCACCTTCAG CGGCCATGTT ATCACCTGGG TGCGACAGGC CCCTGGACAA	120
GGACTTGAGT GGATGGGAGA GAGCATCCCT ATCTTGGTT CCGCAAACCA CGCTCAAAAC	180
TACGCTCAGA AATTCCGGGA CAGAGTCTCG ATTATCGCGG ACGAATCCAC GAGCACGTCG	240
TTCATTGAGC TGAGCAACCT GAGATCTGAC GACACGGCCG TCTACTACTG TGCGAGAGAC	300
CCTCCAAGAT ATTGCAGTGC TGGTAGATGC TACCCGGGAT TCTTCCAGCA GTGGGGCCAG	360
GGCACCCCTCG TCACCGTCTC CTCA	384

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCGAGCAGT CTGGGGCTGA GGTGAAGAAG CCTGGGTCT CGGTGAAGGT CTCCTGTCAG	60
GTTTTTGGAG ACACCTTCAG CAGATACACT ATTCACTGGT TGCGACAGGC CCCTGGACAA	120
GGGCCTGAGT GGATGGGAAA TATCATCCCT GTCTATAATA CACCAAACCA CGCGCAGAAG	180
TTTCAGGGCA GACTCTCGAT AACCGCCGAC GATTCCACGA GCACAGCCTA CATGGAACTG	240
AGTAGCCTCA GATCTGAGGA CACGGCCGTC TATTCTGTG CGAGAGTCGT AATACCAAAT	300
GCAATCCGGC ACACGATGGG ATATTACTTT GACTACTGGG GCCAGGGAAC CCTGGTCACC	360
GTCTCCTCA	369

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTCGAGCAGT CTGGGGCTGA GGTGAAGAAG CCTGGGTCT CAGTGAAGGT CTCCTGCAAG	60
GCTTCTGGAG GCACCTTCAG CGGCCATGTT ATCAGCTGGG TGCGACAGGC CCCTGGACAA	120
GGGCTTGAGT GGATGGGGGG GAGTATCTCT TTCTTGGCA CATCAAACCTC CGCACAGAAG	180
TTCCAGGGCA GAGTCTCGAT TACCGCCGAC GAATCCGCGA GCACAGCCTA CATGGAGCTG	240
AGTAGCCTGA GATCGGAGGA CACGGCCATC TATTACTGTG CGAAAGACCC TCCAAGATTT	300
TGTAGTGGTG GTAACTGCTA CCCGGGGTTC TTCCAGCAGT GGGGCCAGGG CACCCCTGGTC	360
ACCGTCTCCT CA	372

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTCGAGTCGG	GGGGAGGCCT	GGTCCAGCCT	GGGAGGTCCC	TGAGACTCTC	CTGTGCAGCG	60
TCTGGATTCA	CCTTCAAGAC	GTATGGCATG	CACTGGTCC	GCCAGGCTCC	AGGCAAGGGG	120
CTGGAGTGGG	TGGCAGGTAT	TTCGTTGAT	GGAAGTAACC	AATATTACGC	AGACTCCGTG	180
AAGGGCCGAT	TCATCGTCTC	CAGAGACAAT	TCCAGGGACA	CGGTGTTCT	GCAGATGAGC	240
AGCCTGAGAC	TCGAGGGACAC	GGCTGTCTAT	TACTGTGCGA	CAGAGGGTTC	TCCTTTGGC	300
TCGATTAAGG	GGCGTTACTA	CCTTGAAAAT	TGGGCCAGG	GAACCTGGT	CACCGTCTCC	360
TCA						363

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGGTGCAGC	TGCTCGAGTC	GGGCCAGGA	CTGGTGAAGC	CTTCGGGAC	CCTGTCCCTC	60
ACCTGCAGT	TCTCTGGTGG	CTCCATCAGG	AGCAGTCACT	GGTGGAGTTG	GGTCCGCCAG	120
CCCCCAGGGA	AGGGACTGGA	GTGGATTGGA	GAAGTCTTT	TTAGTGGAAAG	CACCATCTAC	180
AACCCATCCC	TCAACGATCG	AGTCTTCATG	TCTGTAGACA	AGTCCAAGGA	CCAGGTCTCC	240
CTGAGGCTGA	GCTCTGTGAC	CGCCGCGGAC	ACGGCCGTGT	ATTACTGTGC	GAGATCCCCC	300
ATAAAAATGA	ATCAGGGAAAG	AATGATGTTG	GATGCCTTG	ATATCTGGGG	CCAGGGGACA	360
CTCGTCATCG	TCTCTTCC					378

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGGTGCAGC	TGCTCGAGTC	TGGGTCTGAG	GTGAAGAAC	CTGGGTCTTC	GGTGAAGGTC	60
TCCTGCAGGG	CCTCTGGAGG	CAGCTTCAGA	AGCTACAATT	TCAATTGGGT	GCGACAGGCC	120
CCTGGACAAG	GTCTTGAGTG	GATGGGAGGC	ATCATCCCTA	TGTTCGGAAC	AGCAAACTAC	180
GCACAGAACT	TTCAGGGCAG	AGTCACAATT	ACCGCGGACG	AATCCACGGC	CACAGGCTAC	240
ATGGAGTTGA	GCAGTCTGAG	ATCTGAAGAC	ACGGCCGTTT	ATTACTGTGC	GATGCCCTAT	300
CCAAAACATT	GCAGTCGTGG	AAGTTGCTGG	GGCTGGTTCG	ACCCCTGGGG	CCAGGGAACT	360
CTGGTCACCG	TGTCTTCA					378

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val	Ala	Gly	Val	Asp	Ala	Ser	Thr	Tyr	Thr	Thr	Gly	Gly	Gln	Ser	Gly
1					5				10				15		
Arg	Thr	Thr	Tyr	Gly	Ile	Val	Gly	Leu	Phe	Ser	Leu	Gly	Pro	Ser	Gln
					20			25				30			
Lys	Leu	Ser	Leu	Ile	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	
					35			40				45			

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAACGCAATT	AATGTGAGTT	AG	22
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(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCCCCTTAT TAGCGTTTGC CATC

24

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATAGAAGTTG TTCAGCAGGC A

21

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AAGACAGCTA TCGCGATTGC AG

22

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTCGTTGACC AGGCAGCCCA G

21

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCTATTGCC TACGGCAGCC G

21